

PR 21-JUL-1997; 97US-0053329.
PR 04-AUG-1997; 97US-0054642.

XX (CMB-) CAMBIA BIOSYSTEMS LLC.
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PI Bowtell D, Killian A;
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DR WPI; 1999-106060/09.
DR P-PSDB; AAY00627.
XX

PT New isolated vertebrate telomerase genes - used to develop products
PT for treating cancers or for organ regeneration, nerve cell or brain
PS cell growth following injury or bone marrow transplantation
PS
XX
XX

Claim 3; Fig 1; 134pp; English.

This sequence encodes the human telomerase of the invention. Primers that amplify the telomerase coding sequence can be used in a method for diagnosing cancer in a patient. The telomerase can be used for detection, diagnosis and drug screening. Inhibitors of telomerase activity can be used to treat cancers such as melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon carcinomas, leukemias, lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin growths. Enhancers of telomerase may be used to stimulate stem cell proliferation and differentiation (expansion of haematopoietic stem cells could be administered in the bone marrow transplant context). As well, many tissues have stem cells. Proliferation of these cells may be useful in wound healing, hair growth, treatment of disease such as Wilms' tumour, organ regeneration or differentiation after injury or diseases, nerve cell or brain cell growth following injury.

Sequence 3964 BP; 661 A; 1337 C; 1257 G; 709 T; 0 other;

alignment_scores:

Quality: 5866.00 Length: 1132
Ratio: 5.247 Gaps: 1
Percent Similarity: 98.763 Percent Identity: 98.763

Alignment block:

US-09-502-424-46 x MAX18254

Align seg 1/1 to: MAX18254 from: 1 to: 3964

1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerH17
1 AAGCCGCGCGCTCCCGCTGCGAGCGCTGCGCTCCCTGCTGCGAGCCA
17 5ThrArgGluValLeuProLeuAlaThrPheValArgArgLeuGlyProG 34
51 CTACCGGAGGTGCTGCGCTGCGCTGCTGCGCTGCGCTGCGCTGCGCTG 100
34 InGlyTPArgLeuValGlnArgGlyAspProAlaAlaPheArgAlaLeu 50
101 AGGGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 150
51 ValAlaGlnCysLeuValCysValProTirPaspAlaArgProProAla 67
151 GGGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 200
67 aAlaProSerPheArgGlnValSerCysLeuGlyGluLeuValAlaArgV 84
201 CCCCCCTCTCCCGCGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 250
84 alLeuGlnArgLeuGlyGlnArgGlyAlaAlaValAlaValAlaValAla 250
251 TGCTGCAAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProGlnAlaAlaPheThrH 117
301 TTCGCGTGTGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 350
117 rSerValArgSerTyrLeuProAsnThrValThrAspAlaLeuArgGlyS 134

351 CAGCGTGCACCTACCTGCTCCCAACAGGCGGACCGACGACCTCGGGGA 400
134 ergAlaAlaTrpGlyLeuLeuLeuArgValAlaGlyAspValLeuVal 150
401 GCGGCGCTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 450
151 HisLeuLeuAlaArgCysAlaLeuPheValLeuValAlaProSerCysAl 167
451 CACCTGCTGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 500
167 aTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAlaAlaThrGlnA 184
501 CTACAGGTGTGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 550
184 laArgProProProAlaSerCysLeuProArgArgArgGlyGlyGly 200
551 CCGGCTG 600
201 ArgAlaTrpAsnHisSerValArgGlyAlaGlyValProLeuGlyLeuP 217
601 CCGGCGCTGGAACCATAGCTGAGGAGGCGCGCGCGCGCGCGCGCGCTG 650
217 oAlaProGlyAlaArgArgGlyGlySerAlaSerArgSerLeuProL 234
651 AGCCCGCGCTGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 700
234 euProLysArgProArgArgGlyAlaAlaProGlnProGlnArgThrPro 250
701 TGCCCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 750
251 ValGlyGlnGlySerTrpAlaHisProGlyArgThrArgGlyProSerAs 267
751 GTTGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
267 ParGlyPheCysValValSerProAlaArgProAlaGlnGlnAlaThrS 284
801 CCGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850
284 erLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
851 CTTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTr 317
901 CGCCAGCACACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 950
317 PaSPThrProCysProProValTyrAlaGlnThrLysHisPheLeuTyrS 334
951 GGACACCGCTTGTCCCGCGGTACGCGCGAGACCAACACCATCTTCTACT 1000
334 erSerGlyAspLysGlnGlnLeuArgProSerPheLeuLeuSerSerLeu 350
1001 CCTCAGCGACAAAGAGACAGCTGCGCGCTCTTCCATCTGAGCTCTGTG 1050
351 ArgProSerLeuThrGlyAlaArgArgLeuValGlnThrLlePheLeuG 367
1051 AGGCCAGCGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1100
367 ySerArgProTrpMetProGlyThrProArgArgLeuProArgLeuPro 384
1101 TTCAGGCGCTGGATGCCAGGAGCTCCCGGAGGTTCGCCCGCTGCGCC 1150
384 InArgTyrTrpGlnMetArgProLeuPheLeuGlnLeuGlnLysAsnHis 400
1151 AGCGCTACTGCAATGCGCGCGCTGTTCTGGAAGCTCTTGGGAAACAC 1200
401 AlAGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAl 417
1201 GCGCAGTGCCTCAAGGGGTGCTCTCAAGACGACATGCGCTGCGAGC 1250
417 aAlaValThrProAlaAlaGlyValCysAlaArgGlyLysProGlnLys 434

1251 TCGGCTCACCCGACGCGGTCTGTGCGCCGGAGAGCCCGAGGCT 1300
434 erValAlaAlaProGluGluGluAspThrAspProArgArgValGln 450
1301 CTGTGGCGGCGCCGAGGAGGAGACACAGACCCCGTGGCTGTGTCAG 1350
451 LeuLeuArgGlnHisSerSerProTyrGlnValTyrGlyPheValArgAl 467
1351 CTGTCTCCGCGACACAGAGCCCGTGGAGGTGTACGGCTGTGCGGCGC 1400
467 ACysLeuArgArgValProProGlyLeuTyrPglySerArgHisAsn 484
1401 CTGCTGGCGCGGTGGTGGCCCGACGCTCTGGGGCTCCAGCGCACAGC 1450
484 LuArgArgPheLeuArgAsnThrTyrLysPheTLeuLeuGlyLysHis 500
1451 AACCGCGCTCTCCAGAACACCAAGAGTTCATCTCCCTGGGGAAGCAT 1500
501 AlaLysLeuSerLeuGlnGluLeuThrTyrPlysMetSerValArgAsp 517
1501 GCCAAGCTCTGCTGACAGAGCTGACGTGAAGATGAGCGCGGGGCTG 1550
517 AlaTyrLeuArgArgSerProGlyValGlyCysValProAlaAlaGlu 534
1551 CGCTGGCTGCGCAGAGACCCAGGGGTGGCTGTCTCCGGCGCAGAGC 1600
534 LsArgLeuArgGluGluLeuAlaLysPheLeuHisTyrLeuMetSer 550
1601 ACCGTGCGCGAGAGATCTGCGCAAGTTCCTGCACTGGCTGTAGAT 1650
551 ValTyrValAlaGluLeuLeuArgSerPhePheTyrValThrGluThr 567
1651 GTGTAGCTCTCGAGCTGCTCGAGGTCTTCTTTATGTACAGAGACAC 1700
567 rPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTyrSerLys 584
1701 GTTTCAAAAGACAGGCTCTTCTTCTACCGAAGAGTGTGGAGCAAGT 1750
584 euGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArg 600
1751 TGCAGAGCATGTGAATCAGACACACTTGAAGAGGTGCGAGCTCGGAG 1800
601 LeuSerGlnAlaGluValArgGlnHisArgGluAlaArgProAlaLeu 617
1801 CTGTGGAGGACAGAGGTCAAGCATCGGGAAGCCAGGCGCGCTGCT 1850
617 uThrSerArgLeuArgPheIleProLysProAspGlyLeuArgProIle 634
1851 GACGTCCAGACTCCGCTTCATCCCAAGCTTGAGGGCTCGGCGCATG 1900
634 AlaSerMetAspTyrValValGlyAlaArgThrPheArgArgGlyLys 650
1901 TGACATGAGCTACGTCTGTGGAGCCAGAACCTTCGACAGAAAAGAG 1950
651 AlaGluArgLeuThrSerArgValLysAlaLeuPheSerValLeuAsn 667
1951 GCCGAGCGCTTCACCTCGAGGGTGAAGGACCTTGAAGGTGTCAACTA 2000
667 rGluArgAlaArgArgProGlyLeuLeuGlyLysSerValLeuGlyLeu 684
2001 CGAGGGGCGGCGCGCCCGCTCTGGGCGCTCTGCTGGGCGCTG 2050
684 spAspIleHisArgAlaTyrPheArgThrPheValLeuArgValArgAla 700
2051 ACGATATCCACAGGCGCGCGACCTTCGCTCGTGTGGGCGCCAG 2100
701 AspProProProGluLeuTyrPheValLys 710
2101 GATCCCGCGCTGAGCTGTACTTGTCAAGGTGATGTGACGGCGCGTA 2150
711 AspArgLeuThrGluValIleAlaSerIleIle 722
2151 CGACACCATCCCGGAGGACAGGCTCAGGAGGTCTATCGCAGACATCA 2200

722 ysProGlnAsnThrTyrCysValAlaArgTyrAlaValAlaGlnLysAla 738
2201 AACCCAGACACAGTACTGTGCGTGGCTGTATGCGGTGTCCAGAGGCG 2250
739 AlaHisGlnHisValArgLysAlaPheLysSerHisValSerThrLeu 755
2251 GCCCATGGGACAGTCCCGCAAGGCTTCAGAACCCAGCTCTTACTGTGAC 2300
755 rAspLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnThrHis 772
2301 AGACCTCAGCGTACATGACAGATTCTGTGCTCACCCTGACAGAGACA 2350
772 erProLeuArgAspAlaValAlaIleGlnGlnSerSerSerLeuAsnGlu 788
2351 GCCCGTAGAGGATGCGTGTGATTCAGACAGAGCTCTCTCTGATATGAG 2400
789 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAl 805
2401 GCCACAGATGGCTCTTGTGACGCTTCTTACGCTTCACTGTGCCACAGC 2450
805 aValArgIleArgGlyLysSerTyrValGlnCysGlnGlyIleProGln 822
2451 CGTGGCATCAGGGGCGCAAGTCTACGTCAGTCCAGGAGGATCCCGCAG 2500
822 LysrIleLeuSerThrLeuLeuCysSerLeuCysTyrGlyAspMetGlu 838
2501 GCTCCATCTCTCAGCGCTCTCTGACGCTGTGCTTACAGCGAGCATGAG 2550
839 AsnLysLeuPheAlaGlyIleArgArgAspGlyLeuLeuLeuArgLeu 855
2551 AACCAAGCTTTTGGCGGGATTCGCGGGAGCGGCGTCTCTGGGTTGGT 2600
855 LAspAspPheLeuValThrProHisLeuThrHisAlaLysThrPhe 872
2601 GGATGATTTCTGTGTGTGACACACTTACCTACCCAGCGCAAAACCTTC 2650
872 euArgThrLeuValArgGlyValProGluTyrGlyCysValAlaLeu 888
2651 TGAGGACCTGTGCGAGGTGTCCGTGATGATGCGCGGTGTGACTG 2700
889 ArgLysThrValAlaAsnPheProValGlnAspLysPheSerTyrAla 905
2701 CGGAGACAGTGTGAATCTCCCTGTAGAACAGAGGCGCTGGGTGGAC 2750
905 rAlaPheValGlnMetProAlaHisGlyLeuPheProTyrCysGlyLeu 922
2751 GCTTTTGTTCAGATGCGGCGCCAGCGGCTATTCCTCTGTGGGCTGC 2800
922 euLeuAspThrArgThrLeuGluValGlnSerAspTyrSerSerTyrAla 938
2801 TGTGAGATACCGGACCTGAGGTGACAGCGACTTACCTCAGCTATGCT 2850
939 ArgThrSerIleArgAlaSerLeuThrPheAsnArgGlyPheLysAla 955
2851 CGGACCTTCATCAGAGCCAGTCTCACCCTTCAACCGGCTTCAAGCTGG 2900
955 YAsnAsnMetArgArgLysLeuPheGlyValIleLeuArgLeuLysHis 972
2901 GAGGACATCGTGCAGAACTCTTGGGGCTTTCGCGCTGAAGGTCTACA 2950
972 erLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 988
2951 GCTGTGTTCTGGATTGTGACGTGAACAGCTCCAGAGGTGTGACCAAC 3000
989 IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLe 1005
3001 ATCTACAAGATCTCTCGTGCAGCGCTTACAGGATGTGTGCT 3050
1005 uGlnLeuProPheHisGlnGlnValTyrPlysAsnProThrPhePheLeu 1022
3051 GAGGCTCCATTTTCATCAGCAAGTTGGAAGAACCCACATTTTCTCTGC 3100

1022 rgVallIeserAspThrAlaSerLeuCysTyrSerIleLeuLysAlaLys 1038
 3101 GGTGATCTCTGTGACAGGCTCCCTCTGCTACTCCATCTGAAAGCCAG 3150
 1039 AsnIaGlyMetSerLeuGlyAlaLysGlyAlaIaGlyProLeuProse 1055
 3151 AACGCAAGGATGTCTGCTGGGGGCCAAGGGCGCGCCGCTCTGCCCTTC 3200
 1055 rGluAlaValGlnTrpLeuGlySHisGlnAlaPheLeuLeuLysLeuThra 1072
 3201 CGAGGCCGCTGAGTGGCTGTGCTGCCACCAAGCATTCCTGCTCAAGCTGACTC 3250
 1072 rGHisAlaGlyValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1088
 3251 GACACCGGTGTACACCTAGTGTCCACTCCTGGGGTCACTCAGGAGACCCAG 3300
 1089 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAl 1105
 3301 ACGCAGCTGAGTCGGAGAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGC 3350
 1105 AlaAlaAsnProAlaLeuProSerAspPheLysThrIleLeuAsp 1120
 3351 CGCAGCCCAACCCGGCCTGCCCTCAGACTTCAGACACATCTCTGGAC 3396